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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/574,735BDATE 09/26/2001
TIME 23:02:37

INPUT SET: S36631

TELECENTER 1600/2900

NOV 13 2001

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This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Ceriani, Roberto L.
6 Peterson, Jerry A.
7 Larocca, David J.
8
9 (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON
10 KIT & METHODS
11
12 (iii) NUMBER OF SEQUENCES: 5
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Ratner & Prestia
16 (B) STREET: Suite 301
17 One Westlakes, Berwyn
18 (C) CITY: Valley Forge
19 (D) STATE: Pennsylvania
20 (E) COUNTRY: USA
21 (F) ZIP: 19482
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk 3.5"
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
27 (D) SOFTWARE: PatentIn #1.0,
28 Version #1.25
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER: 08/482,596
32 (B) FILING DATE: June 7, 1995
33 (C) CLASSIFICATION:
34
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Amzel, Viviana
37 (B) REGISTRATION No.: 30,930
38 (C) REFERENCE/DOCKET No.: CRFC-046
39
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: (610) 407-0700
42 (B) TELEFAX: (610) 407-0701
43 (C) TELEX: N.A.
44
45
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/574,735BDATE: 09/26/2001
TIME: 23:02:37

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47 (2) INFORMATION FOR SEQ ID NO:1:
48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1384 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: both

53 (D) TOPOLOGY: linear
5455 (ii) MOLECULE TYPE: DNA
5657 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58

```
59 GATTTTCATCC ATGATGTTAA TAAAAAACAC AAGGAGTTTG TGGGTAAC TG 50
60 GAACAAAAAC GCGGTGCATG TCAACCTGTT TGAGACCCCT GTGGAGGCTC 100
61 AGTACGTGAG ATTGTACCCC ACGAGCTGCC ACACGGCCTG CACTCTGCGC 150
62 TTTGAGCTAC TGGGCTGTGA GCTGAACGGA TGCGCCAATC CCCTGGGCCT 200
63 GAAGAATAAC AGCATCCCTG ACAAGCAGAT CACGGCCTCC AGCAGCTACA 250
64 AGACCTGGGG CTTGCATCTC TTCAGCTGGA ACCCCTCCTA TGCACGGCTG 300
65 GACAAGCAGG GCAACTTCAA CGCCTGGGTT GCGGGGAGCT ACGGTAACGA 350
66 TCAGTGGCTG CAGGTGGACC TGGGCTCCTC GAAGGAGGTG ACAGGCATCA 400
67 TCACCCAGGG GGCCCGTAAC TTTGGCTCTG TCCAGTTTGT GGCATCCTAC 450
68 AAGGTTGCCT ACAGTAATGA CAGTGCGAAC TGGACTGAGT ACCAGGACCC 500
69 CAGGACTGGC AGCAGTAAGA TCTTCCCTGG CAACTGGGAC AACCCTCCC 550
70 ACAAGAAGAA CTTGTTTGAG ACGCCCATCC TGGCTCGCTA TGTGCGCATC 600
71 CTGCCTGTAG CCTGGCACAA CCGCATCGCC CTGCGCCTGG AGCTGCTGGG 650
72 CTGTTAGTGG CCACCTGCCA CCCCAGGTC TTCTGCTTT CCATGGGCCC 700
73 GCTGCCTCTT GGCTTCTCAG CCCCTTTAAA TCACCATAGG GCTGGGGACT 750
74 GGGGAAGGGG AGGGTGTTCA GAGGCAGCAC CACCACACAG TCACCCCTCC 800
75 CTCCCTCTTT CCCACCCTCC ACCTCTCACG GGCCCTGCCC CAGCCCTTAA 850
76 GCCCCGTCCC CTAACCCCCA GTCCTCACTG TCCTGTTTTT TTAGGCACTG 900
77 AGGGATCTGA GTAGTCTTGG GATGGACAGG AAAGGGCAAA GTAGGGCGTG 950
78 TGGTTTCCCT GCCCTGTCTT GGACCGCCGA TCCCAGGTGC GTGTGTCTCT 1000
79 GTCTCTCCTA GCCCTCTCTT CACACATCAC ATTCCCATGG TGGCCTCAAG 1050
80 AAAGGCCCGG AAGCCCCAGG CTGGAGATAA CAGCCTCTTG CCCGTCGGCC 1100
81 CTGCGTCGGC CCTGGGGTAC CATGTGCCAC AACTGCTGTG GCCCCCTGTC 1150
82 CCAAGACAC TTCCCCTTGT CTCCCTGGTT GCCTCTCTTG CCCCTTGTCC 1200
83 TGAAGCCCAG CGACACAGAA GGGGGTGGG CGGGTCTATG GGGAGAAAGG 1250
84 GAGCGAGGTC AGAGGAGGGC ATGGGTGGC AGGGTGGGCG TTTGGGGCCC 1300
85 TCATGCTGGC TTTTCACCCC AGAGGACACA GGCAGCTTCC AAAATATATT 1350
86 TATCTTCTTC ACGGGAACAAA AAAAAAAAAA ACCG
```

1384

87
88
89
90 (2) INFORMATION FOR SEQ ID NO:2:91
92 (i) SEQUENCE CHARACTERISTICS:

93 (A) LENGTH: 218 amino acids

94 (B) TYPE: amino acid

95 (C) STRANDEDNESS:

96 (D) TOPOLOGY: linear
9798 (ii) MOLECULE TYPE: protein
99

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/574,735BDATE: 09/26/2001
TIME: 23:02:37

INPUT SET: S36631.raw

100 (v) FRAGMENT TYPE:
101
102
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
104
105 Asp Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val
106 1 5 10
107 Gly Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu
108 15 20 25
109 Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser
110 30 35 40
111 Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys
112 45 50 55
113 Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn
114 60 65 70
115 Ser Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys
116 75 80
117 Thr Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala
118 85 90 95
119 Arg Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly
120 100 105 110
121 Ser Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser
122 115 120 125
123 Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn
124 130 135 140
125 Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr
126 145 150
127 Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
128 155 160 165
129 Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His
130 170 175 180
131 Ser His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg
132 185 190 195
133 Tyr Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala
134 200 205 210
135 Leu Arg Leu Glu Leu Leu Gly Cys
136 215
137
138
139
140 (2) INFORMATION FOR SEQ ID NO:3:
141
142 (i) SEQUENCE CHARACTERISTICS:
143 (A) LENGTH: 217
144 (B) TYPE: amino acid
145 (C) STRANDEDNESS:
146 (D) TOPOLOGY: linear
147
148 (ii) MOLECULE TYPE: protein
149
150 (v) FRAGMENT TYPE:
151
152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

RAW SEQUENCE LISTING PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:38

INPUT SET: S36631.raw

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153
154 Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val Gly
155 1 5 10
156 Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu Thr
157 15 20 25
158 Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser Cys
159 30 35 40
160 His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu
161 45 50 55
162 Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser
163 60 65 70
164
165 Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr
166 75 80
167 Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg
168 85 90 95
169 Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly Ser
170 100 105 110
171 Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser Ser
172 115 120 120
173 Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn Phe
174 130 135 140
175 Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr Ser
176 145 150
177 Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg Thr
178 155 160 165
179 Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser
180 170 175 180
181 His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr
182 185 190 195
183 Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu
184 200 205 210
185 Arg Leu Glu Leu Leu Gly Cys
186 215 217
187
188
189

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

202 Phe Lys Gly Asn Ser Thr Arg Asn Val Met Tyr Phe Asn Gly
203 1 5 10
205

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:38

INPUT SET: S36631.raw

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206 Asn Ser Asp Ala Ser Thr Ile Lys Glu Asn Gln Phe Asp Pro
207 15 20 25
208 Pro Ile Val Ala Arg Tyr Ile Arg Ile Ser Pro Thr Arg Ala
209 30 35 40
210 Tyr Asn Arg Pro Thr Leu Arg Leu Glu Leu Gln Gly Cys Glu
211 45 50 55
212 Val Asn Gly Cys Ser Thr Pro Leu Gly Met Glu Asn Gly Lys
213 60 65 70
214 Ile Glu Asn Lys Gln Ile Thr Ala Ser Ser Phe Lys Lys Ser
215 75 80
216 Trp Trp Gly Asp Tyr Trp Glu Pro Phe Arg Ala Arg Leu Asn
217 85 90 95
218 Ala Gln Gly Arg Val Asn Ala Trp Gln Ala Lys Ala Asn Asn
219 100 105 110
220 Asn Lys Gln Trp Leu Glu Ile Asp Leu Leu Lys Ile Lys Lys
221 115 120 125
222 Ile Thr Ala Ile Ile Thr Gln Gly Cys Lys Ser Leu Ser Ser
223 130 135 140
224 Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr Ser Glu Gln
225 145 150
226 Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met Val
227 155 160 165
228 Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val
229 170 175 180
230 Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg
231 185 190 195
232 Val Ile Pro Lys Thr Trp Asn Gln Ser Ile Ala Leu Arg Leu
233 200 205 210
234 Glu Leu Phe Gly Cys Asp Ile Tyr
235 215 218
236
237
238

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

```

242 (A) LENGTH: 218
243 (B) TYPE: amino acid
244 (C) STRANDEDNESS:
245 (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

253 Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly
254 1 5 10
255 Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro
256 15 20 25
257 Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr
258 30 35 40

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/574,735B

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INPUT SET: S36631.raw

Line	Error	Original Text
31	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/482,596

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:39

INPUT SET: S36631.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/574,735BDATE: 09/26/2001
TIME: 23:02:39**INPUT SET: S36631.raw**

Line	Original Text	Corrected Text
9	(ii) TITLE OF THE INVENTION: FUSION PROTE	(ii) TITLE OF INVENTION: FUSION PROTEIN W
37	(B) REGISTRATION No.: 30,930	(B) REGISTRATION NUMBER: 30,930
38	(C) REFERENCE/DOCKET No.:CRFC-046	(C) REFERENCE/DOCKET NUMBER:CRFC-046

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
TIME: 23:02:39

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Line	Error	Original Text
31	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/482,596

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PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
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APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/574,735B

DATE: 09/26/2001
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Line	Original Text	Corrected Text
9	(ii) TITLE OF THE INVENTION: FUSION PROTE	(ii) TITLE OF INVENTION: FUSION PROTEIN W
37	(B) REGISTRATION No.: 30,930	(B) REGISTRATION NUMBER: 30,930
38	(C) REFERENCE/DOCKET No.:CRFC-046	(C) REFERENCE/DOCKET NUMBER:CRFC-046